

SEQUENCE LISTING

<110> Trotta, Christopher R.

<120> TARGETING ENZYMES OF THE tRNA SPLICING  
PATHWAY FOR IDENTIFICATION OF ANTI-FUNGAL AND/OR  
ANTI-PROLIFERATIVE MOLECULES

<130> 10589-034-999

<140> US/10/551,300

<141> 2005-09-27

<150> PCT/US2004/009590

<151> 2004-03-26

<150> 60/458,067

<151> 2003-03-27

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 465

<212> PRT

<213> Homo sapiens

<220>

<223> HsSen2p

<400> 1

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Pro Leu Lys Glu Phe Lys Ile Phe Arg Ala Glu Met Ile Asn Asn Asn  
35 40 45  
Val Ile Val Arg Asn Ala Glu Asp Ile Glu Gln Leu Tyr Gly Lys Gly  
50 55 60  
Tyr Phe Gly Lys Gly Ile Leu Ser Arg Ser Arg Pro Ser Phe Thr Ile  
65 70 75 80  
Ser Asp Pro Lys Leu Val Ala Lys Trp Lys Asp Met Lys Thr Asn Met  
85 90 95  
Pro Ile Ile Thr Ser Lys Arg Tyr Gln His Ser Val Glu Trp Ala Ala  
100 105 110  
Glu Leu Met Arg Arg Gln Gly Gln Asp Glu Ser Thr Val Arg Arg Ile  
115 120 125  
Leu Lys Asp Tyr Thr Lys Pro Leu Glu His Pro Pro Val Lys Arg Asn  
130 135 140  
Glu Glu Ala Gln Val His Asp Lys Leu Asn Ser Gly Met Val Ser Asn  
145 150 155 160  
Met Glu Gly Thr Ala Gly Gly Glu Arg Pro Ser Val Val Asn Gly Asp  
165 170 175  
Ser Gly Lys Ser Gly Gly Val Gly Asp Pro Arg Glu Pro Leu Gly Cys  
180 185 190  
Leu Gln Glu Gly Ser Gly Cys His Pro Thr Thr Glu Ser Phe Glu Lys  
195 200 205  
Ser Val Arg Glu Asp Ala Ser Pro Leu Pro His Val Cys Cys Cys Lys  
210 215 220

Gln Asp Ala Leu Ile Leu Gln Arg Gly Leu His His Glu Asp Gly Ser  
 225                   230                   235                   240  
 Gln His Ile Gly Leu Leu His Pro Gly Asp Arg Gly Pro Asp His Glu  
 245                   250                   255  
 Tyr Val Leu Val Glu Glu Ala Glu Cys Ala Met Ser Glu Arg Glu Ala  
 260                   265                   270  
 Ala Pro Asn Glu Glu Leu Val Gln Arg Asn Arg Leu Ile Cys Arg Arg  
 275                   280                   285  
 Asn Pro Tyr Arg Ile Phe Glu Tyr Leu Gln Leu Ser Leu Glu Glu Ala  
 290                   295                   300  
 Phe Phe Leu Val Tyr Ala Leu Gly Cys Leu Ser Ile Tyr Tyr Glu Lys  
 305                   310                   315                   320  
 Glu Pro Leu Thr Ile Val Lys Leu Trp Lys Ala Phe Thr Val Val Gln  
 325                   330                   335  
 Pro Thr Phe Arg Thr Tyr Met Ala Tyr His Tyr Phe Arg Ser Lys  
 340                   345                   350  
 Gly Trp Val Pro Lys Val Gly Leu Lys Tyr Gly Thr Asp Leu Leu Leu  
 355                   360                   365  
 Tyr Arg Lys Gly Pro Pro Phe Tyr His Ala Ser Tyr Ser Val Ile Ile  
 370                   375                   380  
 Glu Leu Val Asp Asp His Phe Glu Gly Ser Leu Arg Arg Pro Leu Ser  
 385                   390                   395                   400  
 Trp Lys Ser Leu Ala Ala Leu Ser Arg Val Ser Val Asn Val Ser Lys  
 405                   410                   415  
 Glu Leu Met Leu Cys Tyr Leu Ile Lys Pro Ser Thr Met Thr Asp Lys  
 420                   425                   430  
 Glu Met Glu Ser Pro Glu Cys Met Lys Arg Ile Lys Val Gln Glu Val  
 435                   440                   445  
 Ile Leu Ser Arg Trp Val Ser Ser Arg Glu Arg Ser Asp Gln Asp Asp  
 450                   455                   460

Leu  
 465

<210> 2  
 <211> 448  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> HsSen2 variant

<400> 2

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								20		25			30		
Pro	Leu	Lys	Glu	Phe	Lys	Ile	Phe	Arg	Ala	Glu	Met	Ile	Asn	Asn	Asn
								35		40			45		
Val	Ile	Val	Arg	Asn	Ala	Glu	Asp	Ile	Glu	Gln	Leu	Tyr	Gly	Lys	Gly
								50		55			60		
Tyr	Phe	Gly	Lys	Gly	Ile	Leu	Ser	Arg	Ser	Arg	Pro	Ser	Phe	Thr	Ile
								65		70			75		80
Ser	Asp	Pro	Lys	Leu	Val	Ala	Lys	Trp	Lys	Asp	Met	Lys	Thr	Asn	Met
								85		90			95		
Pro	Ile	Ile	Thr	Ser	Lys	Arg	Tyr	Gln	His	Ser	Val	Glu	Trp	Ala	Ala
								100		105			110		
Glu	Leu	Met	Arg	Arg	Gln	Gly	Gln	Asp	Glu	Ser	Thr	Val	Arg	Arg	Ile
								115		120			125		
Leu	Lys	Asp	Tyr	Thr	Lys	Pro	Leu	Glu	His	Pro	Pro	Val	Lys	Arg	Asn
								130		135			140		

Glu	Glu	Ala	Gln	Val	His	Asp	Lys	Leu	Asn	Ser	Gly	Met	Val	Ser	Asn
145						150				155					160
Met	Glu	Gly	Thr	Ala	Gly	Gly	Glu	Arg	Pro	Ser	Val	Val	Asn	Gly	Asp
						165			170						175
Ser	Gly	Lys	Ser	Gly	Gly	Val	Gly	Asp	Pro	Arg	Glu	Pro	Leu	Gly	Cys
						180			185						190
Leu	Gln	Glu	Gly	Ser	Gly	Cys	His	Pro	Thr	Thr	Glu	Ser	Phe	Glu	Lys
						195			200						205
Ser	Val	Arg	Glu	Asp	Ala	Ser	Pro	Leu	Pro	His	Val	Cys	Cys	Cys	Lys
						210			215						220
Gln	Asp	Ala	Leu	Ile	Leu	Gln	Arg	Gly	Leu	His	His	Glu	Asp	Gly	Ser
						225			230			235			240
Gln	His	Ile	Gly	Leu	Leu	His	Pro	Gly	Asp	Arg	Gly	Pro	Asp	His	Glu
						245			250			255			
Tyr	Val	Leu	Val	Glu	Glu	Ala	Glu	Cys	Ala	Met	Ser	Glu	Arg	Glu	Ala
						260			265			270			
Ala	Pro	Asn	Glu	Glu	Leu	Val	Gln	Arg	Asn	Arg	Leu	Ile	Cys	Arg	Arg
						275			280			285			
Asn	Pro	Tyr	Arg	Ile	Phe	Glu	Tyr	Leu	Gln	Leu	Ser	Leu	Glu	Glu	
						290			295			300			
Pro	Leu	Thr	Ile	Val	Lys	Leu	Trp	Lys	Ala	Phe	Thr	Val	Val	Gln	Pro
						305			310			315			320
Thr	Phe	Arg	Thr	Thr	Tyr	Met	Ala	Tyr	His	Tyr	Phe	Arg	Ser	Lys	Gly
						325			330			335			
Trp	Val	Pro	Lys	Val	Gly	Leu	Lys	Tyr	Gly	Thr	Asp	Leu	Leu	Tyr	
						340			345			350			
Arg	Lys	Gly	Pro	Pro	Phe	Tyr	His	Ala	Ser	Tyr	Ser	Val	Ile	Ile	Glu
						355			360			365			
Leu	Val	Asp	Asp	His	Phe	Glu	Gly	Ser	Leu	Arg	Arg	Pro	Leu	Ser	Trp
						370			375			380			
Lys	Ser	Leu	Ala	Ala	Leu	Ser	Arg	Val	Ser	Val	Asn	Val	Ser	Lys	Glu
						385			390			395			400
Leu	Met	Leu	Cys	Tyr	Leu	Ile	Lys	Pro	Ser	Thr	Met	Thr	Asp	Lys	Glu
						405			410			415			
Met	Glu	Ser	Pro	Glu	Cys	Met	Lys	Arg	Ile	Lys	Val	Gln	Glu	Val	Ile
						420			425			430			
Leu	Ser	Arg	Trp	Val	Ser	Ser	Arg	Glu	Arg	Ser	Asp	Gln	Asp	Asp	Leu
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<211> 377

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<223> Sc Sen2p

<400> 3

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Ile	His	Pro	Val	Asp	Asp	Leu	Pro	Glu	Leu	Ile	Leu	His	Asn	Pro	Leu
						20			25						30
Ser	Trp	Leu	Tyr	Trp	Ala	Tyr	Arg	Tyr	Tyr	Lys	Ser	Thr	Asn	Ala	Leu
						35			40			45			
Asn	Asp	Lys	Val	His	Val	Asp	Phe	Ile	Gly	Asp	Thr	Thr	Leu	His	Ile
						50			55			60			
Thr	Val	Gln	Asp	Asp	Lys	Gln	Met	Leu	Tyr	Leu	Trp	Asn	Asn	Gly	Phe
						65			70			75			80
Phe	Gly	Thr	Gly	Gln	Phe	Ser	Arg	Ser	Glu	Pro	Thr	Trp	Lys	Ala	Arg
						85			90			95			

Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly  
     100                     105                     110  
 Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr  
     115                     120                     125  
 Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys  
     130                     135                     140  
 Leu Glu Arg Glu Leu Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp  
     145                     150                     155                     160  
 Glu Glu Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe  
     165                     170                     175  
 Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Gln Asp  
     180                     185                     190  
 Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu  
     195                     200                     205  
 Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Glu Leu Met Pro Val Glu  
     210                     215                     220  
 Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala  
     225                     230                     235                     240  
 Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile  
     245                     250                     255  
 His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His  
     260                     265                     270  
 Gly Trp Cys Val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu  
     275                     280                     285  
 Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly  
     290                     295                     300  
 Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala  
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 Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Glu  
     325                     330                     335  
 Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn  
     340                     345                     350  
 Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Glu Val Leu Tyr Lys  
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 Arg Trp Val Pro Gly Arg Asn Arg Asp  
     370                     375

<210> 4  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Motif of the active site for the 5' splice site of yeast  
       and archaeal tRNA splicing endonuclease

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 Tyr Arg Gly Gly Tyr  
     1                     5